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Matches 396
                                                                                                                    FA7_RABIT STANDARD; PRT; 444 AA. P98139; P79224; 01-FEB-1996 (Rel. 33, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93190306; PubMed-8383365;
Brothers A.B., Clarke B.J., Sheffleld W.P.,
"Complete nucleotide sequence of the cDNA en
factor VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                              TISSUE-Liver;
                                                                                                                                                                                                                                                                                                  REVISION TO 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conversion accelerator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9986;
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     SIMILARITY).

CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-I form factor xa.

SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND BY A DISULFIDE BOND (BY SIMILARITY).

TISSUE SPECIFICITY: PLASMA.
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PROSITE; PS00135;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U77477; AAB37326.1; -. P08709; 1FAK.
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o; IPR001314; Chymotrypsin.
o; IPR000561; EGF-11ke.
o; IPR000742; EGF_2.
o; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001254; Ser_protease_Try.
IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease; Blood coagulation; Zymogen; Glycoprotein; sma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O179; EGF_CA; 1.

V001; EGF_like; 1.

V002; TYP_SPC; 1.

V12; EGF_1; 1.

V22; EGF_1; 1.

V23; EGF_2; 1.

V24; EGF_2; 1.

V25; EGF_2; 1.

V26; EGF_2; 1.

V27; EGF_CA; 1.

V28; EGF_CA; 1.

V29; EGF_CA; 1.
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gla; 1.
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TRYPSIN_DOM; 1.
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FACTOR IXA, OR THROMBIN) (
BY SIMILARITY
BY 
                                                                                                                                                                                                                                                                                                                                                                                                  EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                            SERINE PROTEASE.
CLEAVAGE (BY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR VII LIGHT

    CALCIUM-BINDING
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STANDARD;
PRT;
446 AA
P70375;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41)
Coagulation factor VII precursor (EC 3.4.21)
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Best Local 9
SEQUENCE FROM N.A.

MEDLINE-97127167; PubMed-8972017;
Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
"Nucleotide structure and characterization of the murine blood
"nucleotide structure pace 
                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                           conversion accelerator). F7 OR CF7.
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Rodentia;
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71.9%;
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HYDROXYLATION (BY SIMILARITY).
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N-LINKED (GLCNAC...) (POTENTI
N-LINKED (GLCNAC...) (POTENTI
N-LINKED (GLCNAC...) (POTENTI
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Pred. No. 2.9e
12; Mismatches
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0481ABC4FE5427F8 CRC64;
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3.4.21.21)
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Murinae; Mus
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EGF-like
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PS00135;
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25
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FACTOR IXA IN THE SIMILARITY).
CATALYTIC ACTIVITY
    form factor xa.
SUBUNIT: HETERODIMER OF
                       ACTIVITY: Hydrolyzes one
                                                PRESENCE OF
                                              TISSUE FACTOR
                       Arg-|-Ile
   AND
A HEAVY CHAIN LINKED
                                               AND
                       bond
                                              CALCIUM
                      'n
                      factor X to
                                             (BY
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SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND BY A DISULFIDE BOND (BY SIMILARITY).

TISSUE SPECIFICITY: PLASMA.

PIM. THE VITAMIN K-DEPENDENT, ENZYMATIC CAGE RESIDUES ALLOWS THE MODIFIER CALCIUM (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. ENZYMATIC CAF CARBOXYLATION IED PROTEIN TO OF SOME

FAMILY S1.

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SMART; SM00020; Tryp_SPC; 1.

PROSITE: PS00010; ASX_HYDROXYL; 1.

PROSITE: PS00022: EGF 1; 1.

PROSITE: PS01186; EGF 2; FALSE_NEG.

PROSITE: PS01187; EGF CA; 1.

PROSITE: PS00011; GLU_CARBOXYLATION; 1.

PROSITE: PS00240; TRYPSIN_DOM; 1.

PROSITE: PS00134; TRYPSIN_HLS; 1. PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_Ike; 1.
SMART; SM00009; GLA; 1.
SMART; SM00020; Tryp_SPC; 1. ACT_SITE
ACT Pfam; PF00008; EGF; 2. Pfam; PF00089; trypsin; Pfam; PF00594; gla; 1. EMBL; U66079; AAC33796.1; HSSP; P08709; 1BF9. ase; Serine prote Plasma; Vitamin IPRO01314; Chymotrypsin. Repeat; protease; TRYPSIN_SER; 234 283 385 379 63 102 111 122 143 153 24 41 193 446 76 123 169 194 ; EGF_2. ; EGF_Ca. ; GLA_blood. ; Ser_protease_Try. vitK_dep_GLA. <u>~</u> Se; Blood coagulation; Zymogen; Glycoprotein; ; Calcium-binding; Gamma-carboxyglutamic acid Signal; Hydroxylation. Like. FACTOR IXA, OR
BY SIMILARITY
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SUBSTRATE (BY
SUBSTRATE (BY
SUBSTRATE)
BY SIMILARITY
BY SIMILARITY FACTOR VII LIGHT CHAI FACTOR VII HEAVY CHAI GLA-RICH. EGF-LIKE 1, CALCIUM-E EGF-LIKE 2. SERINE PROTEASE. CLEAVAGE (BY FACTOR X POTENTIAL. OR THROMBIN) CALCIUM-BINDING SIMILARITY) CHAIN XA, FACTOR XIIA, (BY SIMILARITY) (POTENTIAL). acid;

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RESULT FA7—BOV ID FA7—BOV ID FA FA P2 SE BO OC B
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Best Local S
Matches 275
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                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                    FA7_BOVIN STANDARD; PRT; 407 AA. P22457; 01-AUG-1991 (Rel. 19, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Coagulation factor VII (EC 3.4.21.21) (Serum Particular Pa
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                        Takeya H.,
                                                MEDLINE-89008362; PubMed-3049594;
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                 Kawabata S.,
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68.1%;
             Nakagawa K.,
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GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGL
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No. 4.8e-115;
             Yamamichi
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          Miyata
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      THE TENT OF THE PROPERTY OF TH
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DOMAIN
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HSSP; P08709; 1BF9
MERODE:
                                                                                                                                                                      EGF-like
                                                                                                                                                                                                                                       Hydrolase;
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InterPro; IPR000294;
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J. Biol. Chem.
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"Bovine factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
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                                                                                                                                                                                                 Vitamin
Repeat.
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PRINTS; PRO0010; EGFBLODD.

PRINTS; PRO0001; EGFBLODD.

SMART; SM00019; EGF_L1ke; 1.

SMART; SM00009; EGF_11ke; 1.

SMART; SM00009; GLA; 1.

SMART; SM00000; Tryp_SPc; 1.

PROSITE; PS00010; ASX, HYDROXYL; 1.

PROSITE; PS00010; EGF_1: 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00135; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iwanaga S., Nishimura H., Rawabata S., Kisiel W., Hase S., Ikenaka T.,
"A new trisaccharide sugar chain linked to a serine residue in the
first EGF-like domain of clotting factors VII and IX and protein Z.",
Adv. Exp. Med. B.b.l. 281:121-131(1990).

-I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CONVERTED TO FACTOR VIIA BY FACTOR XA, FECTOR XIIA, FACTOR IXA, OR
THROMBIN BY MINOR PROTECLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
BY LIMITED PROTECLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.

-I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-Ile bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN: PRINTS; PR00010; EGFBLOOD. PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hase S., Kawabata S., Nishimura H., Takeya H., Sueyo Miyata T., Iwanaga S., Takao T., Shimonishi Y., Iken "A new trisaccharide sugar chain linked to a serine blood coagulation factors VII and IX.";
J. Blochem. 104:867-868(1988).
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PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
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SUBGUT: HETERODIMER OF A LIGHT CHAIN AND BY A DISULFIDE BOND.
TISSUE SPECIFICITY: PLASMA.
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PF00594; gla; 1.
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EGF_Ca.
EGF_II.
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VitK_dep_GLA.
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                                                                                                                                                 2; Blood coagulation; Zymogen; Glycoprotein;
Calcium-binding; Gamma-carboxyglutamic acid
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FACTOR VII LIGHT OF FACTOR VII HEAVY OF FACTOR VII HEAVY OF GLA-RICH.

EGF-LIKE 1, CALCIL EGF-LIKE 2.
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                    CALCIUM-BINDING
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., Ikenaka T.;
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CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN).
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        update
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     MEROPS; SOI.216; ...
InterPro; IPRO00152; A
InterPro; IPRO00561; E
InterPro; IPRO00561; E
InterPro; IPRO00742; E
InterPro; IPRO01881; E
InterPro; IPRO01283; G
InterPro; IPRO01284; E
InterPro; IPRO01254; V
Pfam; PF00008; EGF; 2.
Pfam; PF00008; trypsin
Pfam; PF000594; y gla; 1.
Pfam; PF000722; CHYMO
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PIR; S15838; S
HSSP; P00742;
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Ogasawara T.,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determinant of viral tropism in chick embryo.";
EMBO J. 9:4189-4195(1990).

-I FUNCTION: Factor xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calclum and phospholipid during blood clotting.
-I FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV, AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 41-55 AND 241-261.
SEQUENCE OF 41-55 AND 241-261.
TISSUE-Allantoic fluid;
MEDLINE-91065352; PubMed-2174359;
MEDLINE-91065352; PubMed-2174359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Chorioallantoic membrane;
MEDLINE-91257322; PubMed-2044767;
Suzuki H., Harada A., Hayashi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagai Y.;
"An endoprotease homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of the virus activating protease embryo. Its identity with the blood clotting factor FEBS Lett. 283:281-285(1991).
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Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
(Virus activating protease) (VAP).
EX.
                                                                                                                                                                                                                                                                                                                                     HORE DISULFIDE BONDS.

TISSUE SPECIFICITY: LIVER AND CHORIOALIANT
PIM: THE VITAMIN K-DEPENDENT, ENZYMATIC CA-
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED
CALCIUM.

CALCIUM.

THE ACTIVATION PEPTIDE IS CLEAVED BY
THE MODIFIED
TO PEPTIDASE FAMILY SI
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CARALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE
HE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF
C ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
                          S15838.
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                                                        BAA00724.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the blood clotting chick embryo.";
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Asx_hydroxyl.
Chymotrypsin.
EGF-1ike.
EGF_2.
EGF_Ca.
EGF_II.
EGF_II.
GLA_blood.
Ser_protease_Try.
VitK_dep_GLA.

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PRINTS; PRO0010; EGFBLOOD.

PRINTS; PRO0001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00069; GLA; 1.

R SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS001186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

"OSITE; PS001187; EGF_CA; 1.

"OSITE; PS00011; GLU_CARBOXYLATION; 1.

"SITE; PS00014; TRYPSIN_DOM; 1.

"ITE; PS00134; TRYPSIN_DOM; 1.

"ITE; PS00135; TRYPSIN_SER; 1.

"ATOCEALN; Hydrolase; Serir"
"Arboxyglutamic aci"
"Zymogen; EGF".
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domain; Repeat.
                                                                      HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILAR:
CHARGE RELAY SYSTEM (BY SIMILARITY.
BY SIMILARITY.
BY
                              76;
                          Score 858.5;
Pred. No. 9.3e
76; Mismatches
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ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POT)
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 RESULT 6
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TISSUE=Liver;
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MEDLINE-85216545; |
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FA10_HUMAN STANDARU P00742; Q14340; 21-JUL-1986 (Rel. 01, 01-OCT-1989 (Rel. 12, I 15-JUN-2002 (Rel. 41, I Coagulation factor X pi
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Fung M.R., Hay C.W., McGillivray R.T.A.;
"Characterization of an almost full-length cDNA coding
blood coagulation factor X.";
Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
  MEDLINE-86221713; PubMed-3011603; Kaul R.K., Hildebrand B., Roberts "Isolation and characterization o
                                                                                                                                                                                                                                                                                                                     MEDIINE-87026600; PubMed-3768336;
Leytus S.P., Foster D.C., Kurachi K., Davie E.W.,
"Gene for human factor X: a blood coagulation factor whose
organization is essentially identical with that of factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-91216473; Publ
Messier T.L., Pittman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Messier T.L., Pittman D.D., Long "Cloning and expression in COS-1 human coagulation factor X."; Gene 99:291-294(1991).
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    debrand B., Roberts characterization of
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CDNA."; Gene 41

cMullen B.A., SEQUENCE OF 41-179

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278. MEDLINE-93360277; PubMed-8355279; MEDLINE-93360277; PubMed-8355279; Padmanabhan K.P., Tulinsky A., Park C.H., Bode Padmanabhan K.P., Tulinsky A., Park C.H., Bode Huber R., Blankenship D.T., Cardin A.D., Kisiel W.; "Structure of human des(1-45) factor Xa at 2.2-A resolution."; J., Mol. Biol. 232:947-966(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278 MEDLINE-98283982; PubMed-9618463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90128299; PubMed-2612918; Jagadeeswaran P., Reddy S.V., Rao K.J., "Cloning and characterization of the 5' encoding human factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES MEDLINE-94062825; PubMed-8243461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (amata K., Kawamoto H., Honma T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moleties in the activation of factor X.";
Eur. J. Blochem. 218:153-163(1993).
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"Complete amino acid sequence of the light chain of human blood coagulation factor X: evidence for identification of residue 63 as beta-hydroxyaspartic acid.";
Biochemistry 22:2875-2884(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIDLINE-84222026; PubMed=6587384;
Leytus S.P., Chung D.W., Kislel W.,
"Characterization of a cDNA coding
Proc. Natl. Acad. Sci. U.S.A. 81:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 115-488 FROM N.A.,
                                                                                                                                                                                                                                                                                         FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood coleting.

CATALYTIC ACTYVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE FORNED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OF
                                                                                                                                                  INTRINSIC PATHWAY), C
SIMILARITY: BELONGS T
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Plasma; sy
PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
                                                                                                                                                                                              PTM: N- AND O-GLYCOS
PTM: THE ACTIVATION
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                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
                                                                                                                                                                                                             N- AND O-GLYCOSYLATED
                                                                                                                                                                                                                                      SPECIFICITY: Plasma; synthesized in the liver. HE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATICN IC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
                                                                                                                                                                                                                                                                                                                                                                                                                                    basis for chemical inhibition of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor X.";
                                                                                                                                               RIVATION PEPTIDE IS CLEAVED BY FATHWAY), OR BY FACTOR VIIA (IN TUBELONGS TO PEPTIDASE FAMILY S1.
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                                                                                                                                                                         FACTOR IXA (IN THE THE EXTRINSIC PATHWAY).
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SMART; SM000069; GLA; 1.
SMART; SM000069; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
R PROSITE; PS001186; EGF_2; 2.
JR PROSITE; PS001187; EGF_CAB; 1.
DR PROSITE; PS00111 GLU_CARBOXYLATION; 1.
DR PROSITE; PS00011 GTRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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InterPro; IPR000561;
InterPro; IPR000742;
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; Chymotrypsin.
; EGF-like.
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VitK_dep_GLA.
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domain; Repeat;
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GAMMA-CARBOXYGLUTAMIC A
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FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTE
                                                                                                                                                                                                                                                                          POTENTIAL.
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roxylation; Calcium-binding; Vitamin
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Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
SEQUENCE:
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SEQUENCE-80056619; PubMed-291916;
Katayama K., Ericsson L.H., Enfield
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"Comparison of amino acid sequence (
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P00741;
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| GKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP
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211
221
                                                                                                                                                                                                                                                                             -KLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                      STANDARD;
                                                                                                                                     * 41,00
X,1,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
322
419
101
110
121
140
                                                                                          Chordata; Craniata; Vertebrata; Eute
Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231
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103
199
211
221
                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%;
                                                                                                                                    Created)
Last sequence
Last annote to (EC 3.4.2)
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                                                                                                                                 L sequence update)
t annotation update)
3.4.21.22) (Christmas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMMA-CARBOXYGLUTAMIC ACID.
HYDROXYLATION.
O-LINKED (GALNAC. .),
O-LINKED (GALNAC. .),
N-LINKED (GLONAC. .),
/FTIG-CAR_000013.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 858.5; DB 1;
Pred. No. 9.5e-60;
6; Mismatches 146;
                                                                                                                                                                                     PRT;
            S.
                               D.L.,
                                                                                                                                                                                     416
           bovine
                                                                                                                                                                                     AA
                                Walsh
                                                                                                                                                                                                                                                           404
           coagulation
                                                                                                                                  factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                    Eutel
                                Neurath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488;
                                                                                                   eostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                    InterPro;
InterPro;
                                                                                                   MEROPS; S01.214; -. GlycoSuiteDB; P00741;
                                                                                                                                 EMBL; J00007; AAA30520.
PIR; A00923; KFBO.
HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [6]
STRUCTURE OF CARBOHYDRATE ON SER-53.
MEDLINE-90130422; PubMed-2105311;
Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka "The structure of (xylose)2glucose-O-serine 53 found in "The structure of (xylose)2glucose-O-serine blood clot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE OF CARBOHYDRATE ON SER-53.

MEDLIXE-91344709; PubMed-2129367;

IWANAGA S., Nishimura H., Kawabata S., Kisiel W., Hase S., I
"A new trisaccharide sugar chain linked to a serine residue
first EGF-like domain of clotting factors VII and IX and pro
Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE OF CARBOHYDRATE ON SER-53.

MEDLINE-8921399; PubMed-3149637;

Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,

Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;

"A new trisaccharide sugar chain linked to a serine residue
blood coagulation factors VII and IX.";
                    InterPro;
                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82272386, PubMed-628728
Choo K.H., Gould K.G., Rees D.J
"Molecular cloning of the gene
Nature 299:178-180(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMullen B.A., Fujikawa K., Kisiel W.;
"The occurrence of beta-hydroxyasparts"
K-dependent blood coagulation zymogens."
Biochem. Biophys. Res. Commun. 115:8-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83308813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Christmas Factor) with that proteins.";
                                                                                                                                                                                                                                                                                                                                                       FORM FACTOR XA.

FORM FACTOR XA.

SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EACLIGHT SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EACLIGHT OF 2 ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.

MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARROXYGLUTAMIC ACID MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARROXYGLUTAMIC ACID MISCELLANEOUS AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. 104:867-868(1988).
                                                                                                                                                                                                                                                                                                                                 (GLA) RESIDUES AND, WITH BEYOND THE GLA DOMAIN. SIMILARITY: BELONGS TO PE SIMILARITY: CONTAINS 2 EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 265:1858-1861(1990).

FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.

CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-1le bond in factor X to
                                                   ; IPRO00152;
; IPRO01314;
; IPRO00561;
                    IPR000742;
IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 51-111 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1 FROM N.A.
, PubMed=6287289;
Rees D.J.G., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation zymogens.";
Res. Commun. 115:8-14(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=6688526;
Chymotrypsin.
EGF-11ke.
EGF_2.
EGF_Ca.
EGF_II.
                                                                                  Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A. 76:4990-4994(1979)
                                                                                                                                                                                                                                                                                                                                  PEPTIDASE FAMILY S1. EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of other vitamin K-dependent plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Brownlee G.G.;
human anti-haemophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
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                                                                                                                                                                                                                                                            he EMBL outst
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due in the
protein Z.";
                                                                                                                                                                                                                                                                                    a collaboration
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of factor
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Best Local S
Matches 167
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CARBOHYD
CARBOHYD
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DISULFID
DISULFID
DISULFID
DISULFID
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PROSITE; PS00010; F
PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS01187; E
PROSITE; PS00111; G
PROSITE; PS00011; G
PROSITE; PS00240; T
                                                                                                                                                                        CARBOHYD
ACT_SITE
ACT_SITE
ACT_SITE
VARIANT
                                                                                                                                                                                                                                                                                                                         DISULFID
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SITE
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002383; GL
InterPro; IPR001254; Se
InterPro; IPR000294; VI
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00001;
SMART; SM00179; 1
SMART; SM00001; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PfinTS; PR00722; CHYMOTRYPS
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                         OD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lemophilia;
             71
                                                                                                  il Similarity
167; Conser
                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00020; Tryp_SPC; 1.
2; PS00010; ASX_HYDROXYL; 1
2; PS00021; EGF_1; 1.
2; PS01186; EGF_2; 2.
2; PS01187; EGF_CA; 1.
    FCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPT
                              GNLERECKEEKCSFEEAREVFENTEKTTEFWKQYVDGDQCESNPCLNGGMCKDDINSYEC
                                                           GSLXRXCKXXQCSFXXARXIFKDAXRTKLEWISYSDGDQCASSPCQNGGSCKDQLQSYIC
                                                                                                                                                           158
168
173
261
222
270
366
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Vitamin K; Gamma-carboxyglutanic; Hydroxylation; Zymogen; EGF-like domain.

1 146 FACTOR IXA (ACTIVE FORM) LIGH
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; EGF_CA; 1.
; EGF_11ke; 1.
; GLA; ·1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLABLOOD.
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TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLU_CARBOXYLATION;
TRYPSIN_DOM; 1.
                                                                                                                                                                       158
168
173
261
222
270
366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasma;
                                                                                                                                                           46785
                                                                                                             38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLA_blood:
Ser_protease_Try.
V1tK_dep_GLA:
                                                                                                                                                         MW;
                                                                                                                                                               HYDROXYLATION
BY SIMILARITY
CHINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY FACTOR XIA).
CLEAVAGE (BY FACTOR XIA).
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine_protease; Calcium-binding;
Serine_protease; Calcium-binding;
                                                                                                             Score 850.5;
Pred. No. 3,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 1, CALCIUM-BINDING EGF-LIKE 2.
                                                                                                                                                     34A7DFE916330662 CRC64;
                                                                                            ed. No. 3.4e
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEASE
                                                                                                             .4e-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ACTIVE FORM) HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ACTIVE FORM) LIGHT CHAIN
                                                                                                                         DB 1;
                                                                                                                      Length
                                                                                           Indels
                                                                                                                      416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                           51;
                                                                                         Gaps
                               71
                                                            70
                                                                                           9
FASULTM FASULT
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   Jagadeeswaran
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FA9_HUMAN STANDARD,
P00740;
21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Dast annotation update)
                                                                                                        Jaye M., de la Salle H., Schamber F., Balland A., Findell A., Tolstoshev P., Lecocq J.P.; "Isolation of a human anti-haemophilic factor IX unique 52-base synthetic oligonucleotide probe de acid sequence of bovine factor IX.", Nucleic Acids Res. 11:2325-2335(1983).
                                                                                                                                                                                                                                                                                     MEDLINE-84236100; PubMed-6329734;
Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.C.
Huddleston J.A., Brownlee G.G.;
"The gene structure of human anti-haemophilic factor IX.";
EMBO J. 3:1053-1060(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.I
Graham J.B., Stafford D.W.;
"Evidence for a prevalent dimorphism in the activ
human coagulation factor IX.";
Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
                          MEDLINE-84300526;
                                                                                                                                                                                                                                             MEDLINE-83220788;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 24:3736-3750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-66000558; Pubmed-2994716;

YOShitake S., Schach B.G., Foster D.C.,

"Nucleotide sequence of the gene for hur
factor B).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                  EQUENCE OF 36-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-85190593; Pubmed-3857619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEQSRRVAQVIIPSTYVPGTT--NHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV
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Matches 161
                                                      "Characterization of a full-length cDNA for rabbit factor x.",
Thromb: Res. 85:503-514(1997).

-I FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
converts prothrombin to thrombin in the presence of factor Va,
calcium and phospholipid during blood clotting.

-I CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
Arg-|-Ile bonds in prothrombin to form thrombin.

-I SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                            15-DEC-1998
15-DEC-1998
15-JUN-2002
Coagulation
                                                                                                                                    MEDLINE-97256311; PubMed-9101642; Pendurth1 U.R., Anderson K.D., James H.L.; "Characterization of a full-length cDNA for rabbit factor X.";
                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolag
                                                                                                                                                                                                                                                                                    FA10_RABIT 
019045;
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_RABIT
                                                                                                                                                                         SEQUENCE FROM N.A.
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Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart "The structure of a Ca(2+)-binding epidermal growth factor-like domain: its role in protein-protein interactions.";
Cell 82:131-141(1995).
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       MORE DISULFIDE BONDS.

PTM: THE VITAMIN K-DEPENDENT, E
GLUTAMIC ACID RESIDUES ALLOWS T
CALCIUM (BY SIMILARITY).

PTM: N- AND O-GLYCOSYLATED (BY
PTM: THE ACTIVATION PEPTIDE IS
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                                                                                                                                                                                                                                                                                                                                                                                         F--SIVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRXVGDSFNITEYMFCAGYSDG
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      AND O-GLYCOS
ACTIVATION
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37, Last sequence 41, Last annotations
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     PEPTIDE
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annotation update)
rsor (EC 3.4.21.6) (Stuart factor).
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Pred. No.
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EMBL;
                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-gorsend an email to license@isb-sib.ch).
                                                                                                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS
                                                                                                                                                                                                           ANOTHER SITE, BEYOND SIMILARITY: BELONGS 1
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                  AF003200;
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                AAB62542.1; -.
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SMART; SMOVE,

PROSITE; PS00012; EGE_1; 1.

R PROSITE; PS01186; EGE_C; 2.

JR PROSITE; PS01187; EGE_CA; 1.

DR PROSITE; PS01187; EGE_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00013; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

Trypsin_ser; serine prote

Trypsin_serine prote PRINTS; PRODOCOL; GLABLOUD.
PRINTS; SMOOLT9; EGE_CA; 1.
SMART; SMOOLT9; EGE_11ke; 1.
R SMART; SMOOLOS; GLA; 1.
R SMART; SMOOLOS; GLA; 1.
R SMART; SMOOLOS; TYP_SPC; 1.
PROSITE; PSOOLOS; TYP_SPC; 1.
PROSITE; PSOOLOS; EGE_1; 1.
DR PROSITE; PSOOLOS; EGE_1; 1.
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DR PROSITE; PSOLOS; EGE_1; 1. MOD_RES MOD_RES MOD_RES MOD_RES MOD_RES DOMAIN DOMAIN MOD_RES MOD_RES MOD_RES DOMAIN MOD_RES Pfam; PF00594; Ptam; PF00089 Pfam; PF00008 InterPro; InterPro; InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; V1tK_dep_GLA. HSSP; P00742; MEROPS; S01.2 nterPro; IPR00074; nterPro; interPro; IPR000152; Asx_hydroxyl. IPR001314; Chymotrypsin. IPR000561; EGF-11ke. IPR000742; EGF_2. 66 65 60 59 56 54 47); trypsin; 1. ; EGF; 20 180 190 232 232 165 165 165 69 99 65 60 59 56 54 47 EGF_Ca. Serine protease; 1 d; Hydroxylation; domain; Repeat. SIMILARITY). GAMMA-CARBOXYGLUTAMIC SIMILARITY). GAMMA-CARBOXYGLUTAMIC ACID GAMMA-CARBOXYGLUTAMIC SIMILARITY). GAMMA-CARBOXYGLUTAMIC SIMILARITY). SIMILARITY).
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FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN
EGGF-LIKE 1, CALCIUM-BINDING (POT GAMMA-CARBOXYGLUTAMIC SIMILARITY) SERINE EGF-LIKE BY SIMILARITY PROTEASE Plasma; Blood coagulation; Calcium-binding; Vitamin ACID ACID ACID ACID ACID ACID ACID ACID (BY (BY (BY (BY (BY (BY (BY AB) (BY (POTENTIAL). ~

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                                             Last sequence update)
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Pred. No. 1.4
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peptide.
J. Biol
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MEDLINE-84185716; PubMed-6546930;
Sugo T., Bjoerk I., Holmgren A., Stenflo J.;

"Calcium-binding properties of bovine factor
carboxyglutamic acid-containing region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bovi
                                                                                                                                                                                                                                                                                                                            MEDLINE-76053121; PubMed-1059122;
Fujikawa K., Titani K., Davie E.W.;
Fujikawa K., Titani K., Davie E.W.;
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Xa-alpha to factor Xa-beta.";
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SEQUENCE OF 41-180.
MEDLINE-80130563; PubMed-6766735;
MEDLINE-80130563; PubMed-6766735;
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MEDLINE-73053314; PubMed-4264286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indue K., Morita T.; "Identification of O-linked oligosaccharide chains in the activation reprides of blood coagulation factor X. The role of the carbohydrate potentials in the activation of factor X.";
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"The occurrence of beta-hydroxyaspartic acid in
"The occurrence of beta-hydroxyaspartic acid in
K-dependent blood coagulation zymogens.";
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MEDLINE-94062825; Pul
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MEDLINE-83308813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Bovine factor X1 (Stuart factor): amino-acid
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                 Chem.
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                 261:4008-4014(1986).
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PubMed=8243461;
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                                                  difference between bovine blood
o tyrosine 18 in the activation
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EMBL: X00673; CAA25286.1; -
PIR: A00925; EXBO.
PDB: 1APO: 31-MAY-94.
PDB: 1CCF: 31-MAY-94.
PDB: 1WHE: 15-MAY-97.
PDB: 1WHF: 15-MAY-97.
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         "The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca2+ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.";

Biochemistry 35:11547-11559(1996).

1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

1- CATALYTIC ACTIVITY: Preferential cleavage: Arg.-Thr and then Arg.-Tile bonds in prothrombin to form thrombin.

1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OF THE THE THE DANGE.
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Trewhella J.;
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Sunnerhagen M., Olah
                                                      GlycoSuiteDB;
InterPro; IPR
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"Three-dimensional structure of the apo form of the N-terminal EGF-like module of blood coagulation factor X as determined by spectroscopy and simulated folding.";
Biochemistry 31:5974-5983(1992).
                                                                               MEROPS; S01.216; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "How an epidermal growth factor (EGF)-like resolution NMR structure of the calcium for like domain in coagulation factor x.";
J. Biol. Chem. 267:19642-19649(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRCTURE BY NMR OF 85-126.
MEDLINE-92406922; PubMed-1527084;
Selander-Sunnerhagen M., Ullner M.,
Stenflo J., Drakenberg T.;
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"IH NMR assignment and secondary structure of the Ca2(+
the amino_terminal epidermal growth factor like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 85-126.
MEDLINE-91084483; PubMed-2261466;
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MEDLINE-92329412; PubMed-1627540;
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PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAISTENTER STACKLUM ALSO BINDS, WITH STRONGER APPINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
S01.42.,
.teDB; P00743; -.
.ripR00152; Asx.hydroxyl.
o; IPR001314; Chymotrypsin.
o; IPR000561; EGF-1ike.
renn00742; EGF_2.
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lah G.A., Stenflo J., Forsen
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the Ca2(+)-free form of
domain in coagulation
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R SMART; SM00069; GLA; 1.

R SMART; SM00069; GLA; 1.

JR SMART; SM00020; Tryp_SPC; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00012; EGF_1; 1.

DR PROSITE; PS00013; EGF_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS000134; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

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Best Local
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                                                                           HQAKRF---TVRVGDRNTEQEEGNEMAHEVEMTVKHSRFVKETYDFDIAVLRLKTPIRFR
                                                                                                        NASKPQG-----RIVGGKVCPKGECPWQVLLL-VNGAQLCGGTLINTIWVVSAAHCF
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IPR000294; VitK_dep_GLA.
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EGF-LIKE 2.
SERIME PROTEASE.
CHARGE RELAY SYSTEM.
GAMMA-CARBOXYGLUTAMIC A
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FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, H.
MAY BE REMOVED BUT IS
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Pred. No. 1.6e-58
0; Mismatches 14
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MGD; MGI:88384; F9:
InterPro; IPR00055; EGF-like.
InterPro; IPR00056; EGF-like.
InterPro; IPR000742; EGF-2:
InterPro; IPR001881; EGF-Ca.
InterPro; IPR001254; Ser_protease_Tr
InterPro; IPR001254; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; trypsin; 1.
Pfam; PF000594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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P16294;
01-AUG-1990
01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                                                                          MEROPS;
                                                                                                                                                                                                                                                                               EMBL; M23109; AAA37629.1; -. EMBL; M26236; AAA37630.1; -. PIR; JQ0419; JQ0419. HSSP; P00740; ICFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90215309; PubMed=2323576;
Wu S.-M., Stafford D.W., Ware J.;
"Deduced amino acid sequence of mouse blood-coagulation factor IX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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F9 OR CF9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PROTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    form factor xa.
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                                                                                                                                                                                                                                                     S01.214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 15, Created)
(Rel. 17, Last sequence update)
(Rel. 41, Last annotation update)
factor IX precursor (EC 3.4.21.22) (Christmas factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                     Ser_protease_Try.
_VitK_dep_GLA.
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Query Match
Best Local S
Matches 169
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PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS0001022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00117; EGF_CA; 1.

PROSITE; PS00104; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                      CARBOHYD
CONFLICT
CONFLICT
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ACT_SITE
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ACT_SITE
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SMART; SM00069;
SMART; SM00020;
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                        Similarity
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459
      Conservative
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313
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                                                                        AA;
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                                                                                      98
265
313
409
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116
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181
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                      37.7%;
39.3%;
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      57;
                                                                                 BY SIMILARITY
BY
   Score 824; DB 1;
Pred. No. 4.4e-57;
7; Mismatches 132
                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC
(BY SIMILARITY).
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CLEAVAGE (BY FACTOR XIA) (I
CLEAVAGE (BY FACTOR XIA) (I
GAMMA-CARBOXYGLUTAMIC ACID
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FACTOR IXA (ACTIVE FORM) HEAVY EGF-LIKE 1, CALCIUM-BINDING (PREFF-LIKE 2)
                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY
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                                                                   EF439C840D6CBClA CRC64;
                                 Length 459
   Indels
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(POTENTIAL).
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   72;
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Gaps
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collaboration

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01-FEB-1991
01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                                TISSUE-Liver;

MEDLINE-8932338; PubMed-2752110;

Evans J.P., Watzke H.H., Ware J.L., Stafford "Molecular cloning of a cDNA encoding canine Blood 74:207-212(1989).
                                                                                                                                                                                                                                                                                                                          MEDLINE=90311364; PubMed=2367529;
Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
Phenotypic correction of factor IX deficiency in sk
hemophilic dogs.";
Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FA9_CANFA
P19540;
                                                                                                                     consequences.
                                                                                                                                                    Evans J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coagulation
                                                                                                                          "Canine hemophilia B
                                                                                                                                                                  MEDLINE-90099303;
                                                                                                                                                                                  VARIANT HEMOPHILIA B GLU-418
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                       C. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VITTA
                  IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFTTYNNMFCAGYREGGKDSCEGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTK 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NITEY -- MFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPFPCGRASISYSSKKITRAETVFSNMDYENSTEAVFIQDDITDGAILNNVTESSESLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99303; Pubwed-2481310;
Brinkhous K.M., Brayer G.D., Reisner H.M., Higophilia B resulting from a point mutation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 17, Created)
  (Rel. 17, Last sequence update)
  (Rel. 41, Last annotation update)
  factor IX precursor (EC 3.4.21.22) (Christmas factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                     87:5173-5177(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                           D.W., High K.A.; factor IX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skin
                                                                                                                             High K.A.;
ith unusual
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                   factor X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
pfam; pro0099; trypsin; 1.
pfam; pro0099; gla; 1.
pfam; pro0099; gla; 1.
pfam; pro0099; glablodb.
prints; pr00070; glablodb.
smart; sm00019; gef_Ca; 1.
smart; sm00019; glab. 1.
smart; sm000020; tryp_SPC; 1.
smart; sm00020; tryp_SPC; 1.
pr051TE; ps00010; ASX_HYDROXYL; 1.
pr051TE; ps00118; EGF_L; 1.
pr051TE; ps001187; EGF_CA; 1.
pr051TE; ps00011; GLU_CARDOXYLATION; 1.
pr051TE; ps000135; TRYPSIN_DM; 1.
pr051TE; ps00135; TRYPSIN_HS; 1.
pr051TE; ps00135; TRYPSIN_HS; 1.
pr051TE; ps00135; TRYPSIN_HS; 1.
pr051TE; ps00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                  Repeat;
             MOD_RES
                                           MOD_RES
                                                                        MOD_RES
                                                                                                        MOD_RES
                                                                                                                                       MOD_RES
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                           Blood coagulation; Plasma;
Hydrolase; Glycoprotein; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M21757; AAA75006.1; -.
EMBL; M33826; AAA30844.1; -.
PIR; A30351; A30351.
HSSP; P00740; ICPH.
MEROPS; S01.214; -.
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                Hemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; V1tK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001881;
InterPro; IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000152; Asx_hydroxyl
InterPro: IPR001314; Chymotrypsin
InterPro: IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THACTIVATION PERTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR OR MORE DISULTIBE BONDS.
DISSEASE: HEMOCHILIA B IS DUE TO DEFECTS IN FACTOR IX.
MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                 Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000561;
IPR000742;
                                                                                                                                                                                                                                                                                                                                                           Hydroxylation;
                                              59
                                                                       56
                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                             lycoprotein; Vitamin
                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                    183
217
452
122
164
452
184
218
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EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLA_blood
                                                                                                                                                                                                                                                                                                                                                                        SER; 1.
Serine protease; Calcium-binding;
acid;
                                                      GAMMA-CARBOXYĞLUTAMIC A
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC A
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC A
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                            2ymogen;
                                                                                                                                                                                                                        ACTIVATION PEPTIDE.

ACTIVATION PEPTIDE.

FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.

EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL EGF-LIKE 2.

SEPTIME 7----
                        GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
        GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                              CLEAVAGE (BY FACTOR XIA) (BY CLEAVAGE (BY FACTOR XIA) (BY GAMMA-CARBOXGLUTAMIC ACID
                                                                                                                                                                                CLEAVAGE (BY FACTOR CLEAVAGE (BY FACTOR
                                                                                                                                                                                                                  SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                         Signal;
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                                                                                                                                                                                                                                                                                                                                                            EGF-like
                                                                                                    ACID
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                                                                                                                                                                                                                                            (POTENTIAL).
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SIMILARITY).

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PRICL ID PRICL
ID PRICL
AC 09GLF
AC 09GLF
DI 16-00
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DI 15-00
DE Vitam
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DE facto
GN PROC.
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Best Local S
Matches 163
                              PRTC_PIG STANDARD; PRT; 459 AA. 09GLP2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Vitamin-K dependent protein C precursor (EC 3. (Autoprothrombin IIA) (Anticoagulant protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
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                        actor XIV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGYVSGWGRVFNKGRSASILQYLKVPLVDRATCLRSTKF----TIYNNMFCAGFHEGG
                                                                                                                                                                                                                                                                                              --SLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGS
                                                                                                                                                                                                                                                                                                                              QKRNVIRTILHHSYNATINKYNHDIALLELDEPLTLNSYVTPICIADREYSN---IFLKF
                                                                                                                                                                                                                                                                                                                                                     QSRRVAQVIIPSTY--VPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRF
                                                                                                                                                                                                                                                                                                                                                                                                           GECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFD-KIKNWRNLIAVLGEHDLSEHDGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPFPCGRVSVPHISMTRTRAETLFSNMDYENSTEVEKILDNVTQPLNDFTRVYGGKDAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WCRAGFEGKNCEL----DVTCNIKNGRCKQFCKLGPDNKVVCSCTTGYQLAEDQRSCEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FCLPAFEGRNCETHKDDQLICVNENGGCEQVCSDHTGTKRSCRCHEGYSLLADGVSCTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
G -> E (IN HEMOPHILIA B).
W: 1F6537C46A6960ED CRC64;
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BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 821; DB 1;
Pred. No. 7.4e-57;
7; Mismatches 133
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BY SIMILARITY.
BY SIMILARITY.
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GAMMA-CARBOXYGLUTAMIC
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                                 3.4.21.69)
C) (Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 452;
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                                 coagulation
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EMBL;
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IPRO00294; VITK_dep

riam; PF00008; EGF; 2.

Pfam; PF00008; EGF; 2.

DR Pfam; PF00099; trypsin; 1.

DR Pfam; PF00594; gla; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

NR SMART; SM00001; EGF; 2.

SMART; SM00001; EGF; 2.

SMART; SM00001; EGF; 2.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00113; GLU_CARBOXYLATION; 1.
PROSITE; PS000134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
Gef-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; InterPro; IPR001314; InterPro; IPR000561; InterPro; IPR001881; InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell. Mol. Life Sci. 58:148-159(2001).

-!- FUNCTION: protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21121490; PubMed=11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame
Kim H.K.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002383; InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P04070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF191307;
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CHARGE RELAY SYSTEM.
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BY SIMILARITY.
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Pred. No. 3.7e-
55; Mismatches
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BY SIMILARITY
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                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to licenseeisb-sib.ch).
                            EMBL; X64336; CAA45617.1;
PIR; S18994; S18994.
PIR; S24312; S24312.
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InterPro;
            MEROPS; SO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Wistar;
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            P04070; 1F
S; S01.218;
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Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
"The cDNA cloning and mRNA expression of rat protein C.";
Biochim. Biophys. Acta 1131:329-332(1992).
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin K dependent protein C precursor (EC 3.4.
(Autoprothrombin IIA) (Anticoagulant protein C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92329550; PubMed=1627650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                      STRONGLY PROMOTED BY THROMBOMODULIN.

TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXLATION OF SGLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBOMODULIN COMPLEX.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                         AND VIIIA.
SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
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DB 1; .9e-53;

Length 461;

Indels

48;

Gaps

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216 156 159 112 101 52

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PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00118; EGF_2; 2.
PROSITE; PS001187; EGF_CA; 1.
PROSITE; PS00111; GLU_CARBOXYLATION
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00240; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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SM00001;
SM00069;
SM00020;
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IPR000561; EGF-11ke.
IPR001881; EGF_Ca.
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1254; Ser_protease_Try.
0294; V1tK_dep_GLA.
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ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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Best Local
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STRAIN-129/SvJ;
MEDLINE-98152576; PubMed-9493582;
NECTON OF THE PROPERTY OF T
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MEDLINE-92316897; PubMed-1618739;
Tada N., Sato M., Tsujimura A., Iwase R.,
"Isolation and characterization of a mous,
J. Biochem. 111:491-495(1992).
STRAIN-BALB/c;
MEDLINE-94318474; PubMed-8043441;
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PRINTS; PRO0701; GLABLOOD.
SMART; SM0010; EGF_1Lke; 1.
SMART; SM00001; EGF_1Lke; 1.
SMART; SM00009; GLA; 1.
SMART; SM00009; GLA; 1.
SMART; SM00000; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00101; ASX_HYDROXYL; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS001187; EGF_CA; 1.
PROSITE; PS00013; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                            InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000361; EGF-1ke.
InterPro; IPR001881; EGF-Ca.
InterPro; IPR002383; GIA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                          EMBL; D10445; BAA01235.1; -
EMBL; AF034569; AAC33795.1;
EMBL; D43755; BAA07812.1; -
PIR; JX0210; JX0210
HSSP; P04070; 1PCU
            SIGNAL
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CHAIN
PEPTIDE
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Pfam; PF00089; tryp;
Pfam; PF00594; gla;
                                                                                   Blood coagulation;
Gamma-carboxygluta
                                                                                               Blood
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MEROPS; S01.218; -.
MGD; MGI:97771; Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Romparative study of partial primary structures of the region of mammalian protein C.";

Br. J. Haematol. 86:590-600(1994).

-i- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS.

IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-i- CATALYTIC ACTIVITY: Degradation of blood coagulation
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                                                                                                                                                                                                                                                         trypsin; 1.
                                                                        Repeat;
                                                                  Glycoprotein; Serine protease;
mic acid; Calcium-binding; Vitamin ;
lepeat; Endothelial cell; Hydrolase;
                BY SIMILARITY.

BY SIMILARITY.

PROTEIN C LIGHT CHAIN (B PROTEIN C HEAVY CHAIN (B ACTIVATION PEPTIDE (BY S
          CLEAVAGE (BY THROMBIN)
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SDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMR
                                                           ELDLDIKEILVHPNYTRSSSDNDIALLRLAQPATLSKTIVPICLPNNGLAQQELTQAGQE
                                                                        EOSRRVAQVIIPSTYVPGTTNHDIÄLLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RF
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